

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:05:08 ; Search time 193 Seconds
(without alignments)
89.436 Million cell updates/sec

Title: US-10-634-740-18
Perfect score: 146
Sequence: 1 ARTKQTARKSTGGKAPRKQLATYKAARKSAP 30

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 146 | 100.0 | 38 | 2 | 024165 nicotiana t |
| 2 | 146 | 100.0 | 39 | 2 | 092167 cricetus |
| 3 | 146 | 100.0 | 48 | 2 | Q7M327 patellina gra |
| 4 | 146 | 100.0 | 48 | 2 | Q7M328 patellina gra |
| 5 | 146 | 100.0 | 48 | 2 | Q7M1P0 encephalart |
| 6 | 146 | 100.0 | 50 | 2 | 06Q4U0 valonia ex |
| 7 | 146 | 100.0 | 50 | 2 | 06Q4U4 valonia pu |
| 8 | 146 | 100.0 | 50 | 2 | 06Q4U6 valonia en |
| 9 | 146 | 100.0 | 50 | 2 | 06Q4U8 valonia co |
| 10 | 146 | 100.0 | 50 | 2 | 06Q4V0 ena montana |
| 11 | 146 | 100.0 | 50 | 2 | 06Q4V2 acanthinula |
| 12 | 146 | 100.0 | 50 | 2 | 06Q4V8 vertigo ant |
| 13 | 146 | 100.0 | 50 | 2 | 06Q4W2 cochlicopa |
| 14 | 146 | 100.0 | 50 | 2 | 06Q4W4 cochlicopa |
| 15 | 146 | 100.0 | 50 | 2 | 06Q4W6 cochlicopa |
| 16 | 146 | 100.0 | 50 | 2 | 06Q4W8 pupilla mus |
| 17 | 146 | 100.0 | 50 | 2 | 06Q4X4 columella e |
| 18 | 146 | 100.0 | 50 | 2 | 06Q4X6 truncatelli |
| 19 | 146 | 100.0 | 50 | 2 | 06Q4X8 azeca gooda |
| 20 | 146 | 100.0 | 50 | 2 | 06Q4Y0 cochlidina |
| 21 | 146 | 100.0 | 50 | 2 | 06Q4Y2 punctum pyg |
| 22 | 146 | 100.0 | 50 | 2 | 06Q4Y4 trichia vil |
| 23 | 146 | 100.0 | 50 | 2 | 06Q4Y6 succinea pu |
| 24 | 146 | 100.0 | 50 | 2 | AA555790 succinea |
| 25 | 146 | 100.0 | 50 | 2 | AA555792 succinea |
| 26 | 146 | 100.0 | 50 | 2 | AA555794 trichia v |
| 27 | 146 | 100.0 | 50 | 2 | AA555796 punctum p |
| 28 | 146 | 100.0 | 50 | 2 | AA555798 cochlidin |
| 29 | 146 | 100.0 | 50 | 2 | AA555800 azeca goo |
| 30 | 146 | 100.0 | 50 | 2 | AA555802 truncatel |
| 31 | 146 | 100.0 | 50 | 2 | AA555804 columella |

| | | | | | |
|----|-----|-------|----|---|--------------------|
| 32 | 146 | 100.0 | 50 | 2 | AA555806 columella |
| 33 | 146 | 100.0 | 50 | 2 | AA555808 columella |
| 34 | 146 | 100.0 | 50 | 2 | AA555810 pupilla m |
| 35 | 146 | 100.0 | 50 | 2 | AA555812 cochlicop |
| 36 | 146 | 100.0 | 50 | 2 | AA555814 cochlicop |
| 37 | 146 | 100.0 | 50 | 2 | AA555816 cochlicop |
| 38 | 146 | 100.0 | 50 | 2 | AA555818 cochlicop |
| 39 | 146 | 100.0 | 50 | 2 | AA555820 vertigo a |
| 40 | 146 | 100.0 | 50 | 2 | AA555822 vertigo a |
| 41 | 146 | 100.0 | 50 | 2 | AA555824 vertigo a |
| 42 | 146 | 100.0 | 50 | 2 | AA555826 acanthinu |
| 43 | 146 | 100.0 | 50 | 2 | AA555828 ena monta |
| 44 | 146 | 100.0 | 50 | 2 | AA555830 valonia |
| 45 | 146 | 100.0 | 50 | 2 | AA555832 valonia |

ALIGNMENTS

| RESULT 1 | | | | | |
|---|--|--------------|------|--------|--|
| ID | 024165 | PRELIMINARY; | PRT; | 38 AA. | |
| AC | 024165; | | | | |
| DT | 01-JAN-1998 (Tremblrel. 05, Created) | | | | |
| DT | 01-JAN-1998 (Tremblrel. 05, Last sequence update) | | | | |
| DT | 01-MAR-2004 (Tremblrel. 26, Last annotation update) | | | | |
| DS | Histone H3 (fragment). | | | | |
| OS | Nicotiana tabacum (Common tobacco). | | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; | | | | |
| OC | lamiales; Solanales; Solanaceae; Nicotiana. | | | | |
| OX | NCBI_TaxID=4097; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=Bright Yellow 2; | | | | |
| RX | (MEDLINE=98292547; PubMed=9628927; | | | | |
| RA | Reichheld J.P.; Gigot C.; Chaubet-Gigot N.; | | | | |
| RT | "Multilevel regulation of histone gene expression during the cell | | | | |
| RT | cycle in plant cells." 26:3255-3262(1998) | | | | |
| RL | (Nucleic Acids Res. 26:3255-3262(1998)) | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=Bright Yellow 2; | | | | |
| RA | Chaubet N.; | | | | |
| RL | Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; Y14195; CAA74582.1; -. | | | | |
| DR | PIR; S56707; S56707. | | | | |
| DR | GO; GO:000786; C:nucleosome; IEA. | | | | |
| DR | GO; GO:0003677; F:DNA binding; IEA. | | | | |
| DR | GO; GO:007001; P:chromosome organization and biogenesis (gen. .; IEA. | | | | |
| DR | GO; GO:006634; P:nucleosome assembly; IEA. | | | | |
| DR | InterPro; IPR009072; Histone-H3. | | | | |
| DR | InterPro; IPR00164; Histone_H3. | | | | |
| DR | PRINTS; PR00622; HISTONEH3. | | | | |
| DR | PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1. | | | | |
| FT | NOV_TER 38 | | | | |
| FT | NOV_TER 38 | | | | |
| SQ | SEQUENCE 38 AA; 3939 MW; E1600FC8D9EDD8D3 CRC64; | | | | |
| Query Match 100.0%; Score 146; DB 2; Length 38; | | | | | |
| Best local Similarity 100.0%; Pred. No. 1e-12; | | | | | |
| Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | |
| QY | 1 ARTKQTARKSTGGKAPRKQLATYKAARKSAP 30 | | | | |
| DB | 2 ARTKQTARKSTGGKAPRKQLATYKAARKSAP 31 | | | | |
| RESULT 2 | | | | | |
| ID | 092167 | PRELIMINARY; | PRT; | 39 AA. | |
| AC | 092167; | | | | |
| DT | 01-MAY-1999 (Tremblrel. 10, Created) | | | | |

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DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
GN H3.2 protein (Fragment).
OS Cricetus sp.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10031,
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87315341, PubMed=3627229,
RA Artshkevsky A., Wooden S., Sharma A., Resendez E.Jr., Lee A.S.;
RT "Cell-cycle regulatory sequences in a hamster histone promoter and
RL their interactions with cellular factors.",
DR Nature 328:823-827(1987).
EMBL; M28265; AAA42371.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. ., IEA.
DR InterPro; IPR009072; Histone-fold.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 39
SQ SEQUENCE 39 AA; 4036 MW; DA31600FC8DEDD8 CRC64;

Query Match 100.0%; Score 146; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
DB 2 ARTKOTARKSTGKAPRKQATKARKSAP 31

RESULT 3
QY 07M327 PRELIMINARY; PRT; 48 AA.
AC 07M327;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Histone H3 (Fragment).
OS Patechinus angulosus (Angulate sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Echinidae; Patechinus.
OX NCBI_TaxID=7658;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.",
RL FEBS Lett. 40:167-172(1974).
PIR; A61286; A61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. ., IEA.
DR InterPro; IPR00164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 48
SQ SEQUENCE 48 AA; 5056 MW; 8C4505BF726ESD38 CRC64;

Query Match 100.0%; Score 146; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
DB 1 ARTKOTARKSTGKAPRKQATKARKSAP 30

RESULT 4
QY 07M328 PRELIMINARY; PRT; 48 AA.
AC 07M328;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Histone H3 (Fragment).
OS Pateella granatina (Sandpiper limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Eogastropoda; Docoglossa;
OC Patellicina; Patelloidea; Patellicidae; Pateilla.
OX NCBI_TaxID=6464;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.",
RL FEBS Lett. 40:167-172(1974).
PIR; B61286; B61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. ., IEA.
DR InterPro; IPR00164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 48
SQ SEQUENCE 48 AA; 5056 MW; 8C4505BF726ESD38 CRC64;

Query Match 100.0%; Score 146; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
DB 1 ARTKOTARKSTGKAPRKQATKARKSAP 30

RESULT 5
QY 07M1P0 PRELIMINARY; PRT; 48 AA.
AC 07M1P0;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Histone H3 (Fragment).
OS Eucephalartos caffer (Kaffir bread).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Cycadophyta; Cycadales; Zamiales; Eucephalartos.
OX NCBI_TaxID=36013;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.",
RL FEBS Lett. 40:167-172(1974).
PIR; C61286; C61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. ., IEA.
DR InterPro; IPR00164; Histone_H3.
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QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
DB 1 ARTKOTARKSTGKAPRKQATKARKSAP 30

RESULT 4
QY 07M328 PRELIMINARY; PRT; 48 AA.
AC 07M328;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Histone H3 (Fragment).
OS Pateilla granatina (Sandpiper limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Eogastropoda; Docoglossa;
OC Patellicina; Patelloidea; Patellicidae; Pateilla.
OX NCBI_TaxID=6464;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.",
RL FEBS Lett. 40:167-172(1974).
PIR; B61286; B61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. ., IEA.
DR InterPro; IPR00164; Histone_H3.

RESULT 5
QY 07M1P0 PRELIMINARY; PRT; 48 AA.
AC 07M1P0;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Histone H3 (Fragment).
OS Eucephalartos caffer (Kaffir bread).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Cycadophyta; Cycadales; Zamiales; Eucephalartos.
OX NCBI_TaxID=36013;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.",
RL FEBS Lett. 40:167-172(1974).
PIR; C61286; C61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. ., IEA.
DR InterPro; IPR00164; Histone_H3.
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DR PRINTS: PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON_TER 1 48 1
FT NON_TER 48 48
SQ SEQUENCE 48 AA; 5056 MW; 8C4505BF726ESD38 CRC64;

Query Match 100.0%; Score 146; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 6
Q6Q4U0 PRELIMINARY; PRT; 50 AA.
ID Q6Q4U0
AC Q6Q4U0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Histone H3 (Fragment).
OS Vallonia excentrica.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orchuethra; Pupilloidea; Valloniidae; Vallonia.
CX NCBI_TaxID=145447;
RN [1]
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEb-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559169; AAS55838.1; -
DR InterPro; IPR009072; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 7
Q6Q4U4 PRELIMINARY; PRT; 50 AA.
ID Q6Q4U4
AC Q6Q4U4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Histone H3 (Fragment).
OS Vallonia pulchella.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orchuethra; Pupilloidea; Valloniidae; Vallonia.
CX NCBI_TaxID=229284;
RN [1]
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEb-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559167; AAS55834.1; -
DR InterPro; IPR009072; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;
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Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 8
Q6Q4U6 PRELIMINARY; PRT; 50 AA.
ID Q6Q4U6
AC Q6Q4U6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Histone H3 (Fragment).
OS Vallonia enliensis.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orchuethra; Pupilloidea; Valloniidae; Vallonia.
CX NCBI_TaxID=229285;
RN [1]
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEb-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559166; AAS55832.1; -
DR InterPro; IPR009072; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 9
Q6Q4U8 PRELIMINARY; PRT; 50 AA.
ID Q6Q4U8
AC Q6Q4U8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Histone H3 (Fragment).
OS Vallonia costata.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orchuethra; Pupilloidea; Valloniidae; Vallonia.
CX NCBI_TaxID=145157;
RN [1]
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEb-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559165; AAS55830.1; -
DR InterPro; IPR009072; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
```

Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 10

06Q4V0
ID 06Q4V0 PRELIMINARY; PRT; 50 AA.
AC 06Q4V0 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Histone H3 (Fragment).
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Snoidae; Enidae; Eua.
OX NCBI_TaxID=265227;
RN (1)
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559164; AA555828.1; -
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR000164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 11

06Q4V2
ID 06Q4V2 PRELIMINARY; PRT; 50 AA.
AC 06Q4V2 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Histone H3 (Fragment).
OS Acanthinula aculeata.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orthurethra; Pupilloidea; Valloniidae; Acanthinula.
OX NCBI_TaxID=229287;
RN (1)
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559163; AA555826.1; -
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR000164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 12

06Q4V8
ID 06Q4V8 PRELIMINARY; PRT; 50 AA.
AC 06Q4V8 (TREMBlrel. 27, Created)

RESULT 13

05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Histone H3 (Fragment).
OS Vertigo antiverligo.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orthurethra; Pupilloidea; Vertiginidae; Vertigo.
OX NCBI_TaxID=145162;
RN (1)
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559160; AA555820.1; -
DR EMBL; AY559161; AA555822.1; -
DR EMBL; AY559162; AA555824.1; -
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR000164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 14

06Q4W2
ID 06Q4W2 PRELIMINARY; PRT; 50 AA.
AC 06Q4W2 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Histone H3 (Fragment).
OS Cochlicopa lubrica.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Orthurethra; Cochlicopidae; Cochlicopa.
OX NCBI_TaxID=82567;
RN (1)
RP SEQUENCE FROM N.A.
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY559158; AA555816.1; -
DR EMBL; AY559159; AA555818.1; -
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR000164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 50
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 14

06Q4W4
ID 06Q4W4 PRELIMINARY; PRT; 50 AA.
AC 06Q4W4 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Histone H3 (Fragment).

OS Cochlicopa lubricella.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Orchuethra; Cochlicopidae; Cochlicopidae; Cochlicopa.
 CX NCBI_TaxID=82566;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY559157; AAS55814.1; -.
 DR InterPro; IPR009072; Histone-Fold.
 DR InterPro; IPR00164; Histone_H3.
 DR PRINTS; PR00622; HISTONEH3.
 DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
 FT NON TER 50
 SQ SEQUENCE 50 AA; 5343 MW; 54151831D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
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 Db 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

RESULT 15

ID . Q6Q4W6 PRELIMINARY; PRT; 50 AA.
 AC Q6Q4W6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Histone H3 (fragment).
 OS Cochlicopa nitens.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Orchuethra; Cochlicopidae; Cochlicopidae; Cochlicopa.
 CX NCBI_TaxID=82566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY559156; AAS55812.1; -.
 DR InterPro; IPR009072; Histone-Fold.
 DR InterPro; IPR00164; Histone_H3.
 DR PRINTS; PR00622; HISTONEH3.
 DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
 FT NON TER 50
 SQ SEQUENCE 50 AA; 5343 MW; 54151831D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
 |||
 Db 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

Search completed: December 23, 2004, 11:22:04
 Job time : 194 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:16:09 ; Search time 38 seconds

(without alignments)
52.356 Million cell updates/sec

Title: US-10-634-740-18

Perfect score: 446

Sequence: 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 146 | 100.0 | 72 | 4 | US-09-621-976-7473 |
| 2 | 146 | 100.0 | 108 | 4 | US-09-513-999C-5370 |
| 3 | 146 | 100.0 | 136 | 4 | US-09-621-976-7472 |
| 4 | 146 | 100.0 | 136 | 4 | US-09-976-594-1029 |
| 5 | 142 | 97.3 | 152 | 4 | US-09-248-786A-18649 |
| 6 | 99 | 67.8 | 20 | 3 | US-09-451-034-13 |
| 7 | 99 | 67.8 | 20 | 4 | US-09-876-221-7 |
| 8 | 99 | 67.8 | 20 | 4 | US-09-589-892B-19 |
| 9 | 64 | 43.8 | 13 | 3 | US-09-451-034-8 |
| 10 | 58.5 | 40.1 | 214 | 3 | US-09-041-889-27 |
| 11 | 58.5 | 40.1 | 214 | 3 | US-09-417-264-27 |
| 12 | 58 | 39.7 | 12 | 3 | US-09-451-034-7 |
| 13 | 56 | 38.4 | 93 | 4 | US-09-270-767-39947 |
| 14 | 56 | 38.4 | 93 | 4 | US-09-270-767-55164 |
| 15 | 54 | 37.0 | 375 | 1 | US-08-363-255-7 |
| 16 | 54 | 37.0 | 528 | 1 | US-08-363-255-14 |
| 17 | 54 | 37.0 | 530 | 1 | US-08-363-255-2 |
| 18 | 54 | 37.0 | 530 | 1 | US-08-363-255-3 |
| 19 | 54 | 37.0 | 530 | 1 | US-08-363-255-8 |
| 20 | 54 | 37.0 | 530 | 1 | US-08-363-255-9 |
| 21 | 54 | 37.0 | 530 | 1 | US-08-363-255-10 |
| 22 | 52.5 | 36.0 | 442 | 1 | US-08-363-255-4 |
| 23 | 52.5 | 36.0 | 442 | 1 | US-08-363-255-11 |
| 24 | 52 | 35.6 | 156 | 4 | US-09-252-991A-23987 |
| 25 | 52 | 35.6 | 223 | 3 | US-09-095-855-201 |
| 26 | 52 | 35.6 | 223 | 4 | US-09-205-426-201 |
| 27 | 51.5 | 35.3 | 302 | 4 | US-09-252-991A-19529 |

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| 28 | 51 | 34.9 | 96 | 4 | US-09-252-991A-26685 | Sequence 26685, A |
| 29 | 51 | 34.9 | 236 | 4 | US-09-252-991A-18461 | Sequence 18461, A |
| 30 | 51 | 34.9 | 310 | 1 | US-08-363-255-6 | Sequence 6, Appli |
| 31 | 51 | 34.9 | 445 | 1 | US-08-363-255-5 | Sequence 5, Appli |
| 32 | 51 | 34.9 | 445 | 1 | US-08-363-255-12 | Sequence 12, Appli |
| 33 | 50.5 | 34.6 | 783 | 4 | US-09-252-991A-18035 | Sequence 18035, A |
| 34 | 50 | 34.2 | 144 | 4 | US-09-252-991A-17329 | Sequence 17329, A |
| 35 | 50 | 34.2 | 191 | 4 | US-10-101-664A-753 | Sequence 753, App |
| 36 | 50 | 34.2 | 614 | 4 | US-09-252-991A-28630 | Sequence 28630, A |
| 37 | 50 | 34.2 | 697 | 4 | US-09-252-991A-24009 | Sequence 24009, A |
| 38 | 49.5 | 33.9 | 100 | 4 | US-09-621-976-6834 | Sequence 6834, Ap |
| 39 | 49.5 | 33.9 | 409 | 4 | US-09-252-991A-20892 | Sequence 20892, A |
| 40 | 49 | 33.6 | 13 | 3 | US-09-451-034-3 | Sequence 3, Appli |
| 41 | 49 | 33.6 | 269 | 4 | US-09-408-020-6 | Sequence 6, Appli |
| 42 | 49 | 33.6 | 507 | 4 | US-09-252-991A-31473 | Sequence 31473, A |
| 43 | 49 | 33.6 | 580 | 4 | US-08-311-731A-289 | Sequence 289, App |
| 44 | 49 | 33.6 | 1788 | 2 | US-08-962-284-2 | Sequence 2, Appli |
| 45 | 48.5 | 33.2 | 176 | 4 | US-09-252-991A-17546 | Sequence 17546, A |

ALIGNMENTS

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RESULT 1
US-09-621-976-7473
; Sequence 7473, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OR INVENTION: ESTE and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7473
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa = Gly,Arg,Tyr
US-09-621-976-7473
Query Match 100.0%; Score 146; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31
RESULT 2
US-09-513-999C-5370
; Sequence 5370, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OR INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, RRG
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm

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/ SEQ ID NO 5370
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 89
/ OTHER INFORMATION: Xaa=Ala or Pro
/ NAME/KEY: UNSURE
/ LOCATION: 99
/ OTHER INFORMATION: Xaa=Ala or Leu or Ser or Val
US-09-513-999C-5370
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Query Match
Best Local Similarity 100.0%; Score 146; DB 4; Length 108;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQIARKSTGGKAPRKQLATYKARKSAP 30
Db 2 ARTKQIARKSTGGKAPRKQLATYKARKSAP 31
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RESULT 3
US-09-621-976-7472
/ Sequence 7472, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Ubert, S.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 7472
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 89
/ OTHER INFORMATION: Xaa = Ala,Pro
/ NAME/KEY: UNSURE
/ LOCATION: 99
/ OTHER INFORMATION: Xaa = Asn,Tyr
US-09-621-976-7472
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Query Match
Best Local Similarity 100.0%; Score 146; DB 4; Length 136;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQIARKSTGGKAPRKQLATYKARKSAP 30
Db 2 ARTKQIARKSTGGKAPRKQLATYKARKSAP 31
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RESULT 4
US-09-976-594-1029
/ Sequence 1029, Application US/09976594
/ Patent No. 6673549
/ GENERAL INFORMATION:
/ APPLICANT: Furness, Michael
/ APPLICANT: Buchbinder, Jenny
/ TITLE OF INVENTION: GENES EXPRESSED IN C3A LAYER CELL CULTURES TREATED WITH STEROIDS
/ FILE REFERENCE: PA-0041 US
/ CURRENT APPLICATION NUMBER: US/09/976,594
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/240,409
/ PRIOR FILING DATE: 2000-10-12
/ NUMBER OF SEQ ID NOS: 1143
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/ SOFTWARE: PERL Program
/ SEQ ID NO 1029
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6673549 4832672CD1
US-09-976-594-1029
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Query Match
Best Local Similarity 100.0%; Score 146; DB 4; Length 136;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQIARKSTGGKAPRKQLATYKARKSAP 30
Db 2 ARTKQIARKSTGGKAPRKQLATYKARKSAP 31
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RESULT 5
US-09-248-796A-18649
/ Sequence 18649, Application US/09248796A
/ Patent No. 6747137
/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstein et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ PRIOR FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 18649
/ LENGTH: 152
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-18649
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Query Match
Best Local Similarity 97.3%; Score 142; DB 4; Length 152;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQIARKSTGGKAPRKQLATYKARKSAP 30
Db 18 ARTKQIARKSTGGKAPRKQLATYKARKSAP 47
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```
RESULT 6
US-09-451-034-13
/ Sequence 13, Application US/09451034
/ Patent No. 6369030
/ GENERAL INFORMATION:
/ APPLICANT: Cole, Philip et al
/ TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES
/ FILE REFERENCE: 600-1-265
/ CURRENT APPLICATION NUMBER: US/09/451,034
/ PRIOR FILING DATE: 1999-11-29
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
/ OTHER INFORMATION: MOLECULE THAT ACT AS ENZYME INHIBITOR
/ OTHER INFORMATION: The A in position 1 is a modified residue and is
/ OTHER INFORMATION: acetylated. The K in position 4 is a modified
/ OTHER INFORMATION: residue and is conjugated via its epsilon NH2
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OTHER INFORMATION: group to coenzyme A.
US-09-451-034-13

Query Match 67.8%; Score 99; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGCAAPRKOL 20
DB 1 ARTKOTARKSTGCAAPRKOL 20

RESULT 7
US-09-876-221-7

Sequence 7, Application US/09876221
Patent No. 6555329
GENERAL INFORMATION:
APPLICANT: Jenuwein, Thomas
APPLICANT: Rea, Stephen
APPLICANT: Eisenhaber, Frank
APPLICANT: O'Carroll, Donal
TITLE OF INVENTION: Method for identifying compounds altering higher-order chromatin
FILE REFERENCE: 0652.2240001
CURRENT APPLICATION NUMBER: US/09/876,221
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: EP 00 112 345.4
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: EP 00 112 479.1
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 60/224,220
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-221-7

Query Match 67.8%; Score 99; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGCAAPRKOL 20
DB 1 ARTKOTARKSTGCAAPRKOL 20

RESULT 8
US-09-589-892B-19
Sequence 19, Application US/09589892B
Patent No. 6689583
GENERAL INFORMATION:
APPLICANT: Jenuwein, Thomas
APPLICANT: Laible, Gutz
APPLICANT: O'Carroll, Donal
APPLICANT: Eisenhaber, Frank
APPLICANT: Rea, Stephen
TITLE OF INVENTION: Chromatin-Regulator Genes
FILE REFERENCE: 0652.1670001
CURRENT APPLICATION NUMBER: US/09/589,892B
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 08/945,988
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: PCT/EP96/01818
PRIOR FILING DATE: 1996-05-02
PRIOR APPLICATION NUMBER: DE 195 16 776.7
PRIOR FILING DATE: 1995-05-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 20

TYPE: PRT
ORGANISM: Homo sapiens
US-09-589-892B-19

Query Match 67.8%; Score 99; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGCAAPRKOL 20
DB 1 ARTKOTARKSTGCAAPRKOL 20

RESULT 9
US-09-451-034-8

Sequence 8, Application US/09451034
Patent No. 6369030
GENERAL INFORMATION:
APPLICANT: Cole, Phillip et al
TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES
FILE REFERENCE: 600-1-265
CURRENT APPLICATION NUMBER: US/09/451,034
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PART OF
OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS
OTHER INFORMATION: The first ala is a modified residue; it is
OTHER INFORMATION: acetylated.
US-09-451-034-8

Query Match 43.8%; Score 64; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGCG 13
DB 1 ARTKOTARKSTGCG 13

RESULT 10
US-09-041-889-27
Sequence 27, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-889-27

Query Match 40.1%; Score 58.5; DB 3; Length 214;
Best Local Similarity 55.2%; Pred. No. 0.58;
Matches 16; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 ARTKOTARKSTGKAPKQKATKARKSA 29
DB 130 AATKAPAKKA-ATKAPAKKATKAPAKKA 157

RESULT 11
US-09-417-264-27
Sequence 27, Application US/09417264
Patent No. 6537768
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Conavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-417-264-27

Query Match 40.1%; Score 58.5; DB 4; Length 214;

Best Local Similarity 55.2%; Pred. No. 0.58;
Matches 16; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 ARTKOTARKSTGKAPKQKATKARKSA 29
DB 130 AATKAPAKKA-ATKAPAKKATKAPAKKA 157

RESULT 12
US-09-451-034-7
Sequence 7, Application US/09451034
Patent No. 6369030
GENERAL INFORMATION:
APPLICANT: Cole, Philip et al
TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-265
CURRENT APPLICATION NUMBER: US/09/451,034
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PART OF
OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS
OTHER INFORMATION: The first ala is a modified residue; it is
US-09-451-034-7

Query Match 39.7%; Score 58; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTG 12
DB 1 ARTKOTARKSTG 12

RESULT 13
US-09-270-767-39947
Sequence 39947, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39947
LENGTH: 93
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-39947

Query Match 38.4%; Score 56; DB 4; Length 93;
Best Local Similarity 46.2%; Pred. No. 0.55;
Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPKQKATKARKSA 26
DB 6 AKTHQAKKVVSPQDPRRLTTWVAR 31

RESULT 14
US-09-270-767-55164
Sequence 55164, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:

APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-084
 CURRENT APPLICATION NUMBER: US/09/270,767
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: Patentn Ver. 2.0
 SEQ ID NO 55164
 LENGTH: 93
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-55164

Query March 38.4%; Score 56; DB 4; Length 93;
 Best Local Similarity 46.2%; Pred. No. 0.55;
 Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRRKQLATKAAR 26
 DB 6 AKTHQAAKKVLSPPDPRRQLTTWVAR 31

RESULT 15
 US-08-363-255-7
 Sequence 7, Application US/08363255
 Patent No. 5783386
 GENERAL INFORMATION:
 APPLICANT: JACOBS, Jr., WILLIAM R.
 APPLICANT: BLOOM, BARRY R.
 APPLICANT: COLLINS, DESMOND M.
 APPLICANT: de LISLE, GEOFFREY W.
 APPLICANT: PASCOPELLA, LISA
 APPLICANT: KAKAKAMI, RIKU P.
 TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESSES:
 ADDRESSER: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363,255
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, GLADYS H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 25237-20002.22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 375 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-363-255-7

Query March 37.0%; Score 54; DB 1; Length 375;
 Best Local Similarity 44.4%; Pred. No. 4.8;
 Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
 QY 4 KQTARKSTGGKAPRRKQLATKAAR 30

DB 36 KRTAKASGSPPAKRAATKPAARVXP 62

Search completed: December 23, 2004, 11:35:52
 Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:04:22 / Search time 159 Seconds
(without alignments)
67.685 Million cell updates/sec

Title: US-10-634-740-18

Perfect score: 146
Sequence: 1 ARTKQTARKSTGGAPRKQLATKARKSAP 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_GeneSeq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 146 | 100.0 | 30 | 6 ADA13508 | AdA13508 Human H3 |
| 2 | 146 | 100.0 | 30 | 8 ADO21849 | AdO21849 Human his |
| 3 | 146 | 100.0 | 40 | 5 ABB07291 | ABO07291 Human his |
| 4 | 146 | 100.0 | 40 | 8 ADO21832 | AdO21832 Human his |
| 5 | 146 | 100.0 | 55 | 5 AAU70897 | AAU70897 Histone 2 |
| 6 | 146 | 100.0 | 65 | 3 AAG07049 | AAG07049 Arabidops |
| 7 | 146 | 100.0 | 70 | 2 AAR46075 | Aar46075 Histone H |
| 8 | 146 | 100.0 | 81 | 3 AAG35461 | Aag35461 Arabidops |
| 9 | 146 | 100.0 | 90 | 3 AAG22671 | Aag22671 Zea may |
| 10 | 146 | 100.0 | 93 | 5 ABP42906 | ABP42906 Human ova |
| 11 | 146 | 100.0 | 95 | 3 AAG13239 | Aag13239 Arabidops |
| 12 | 146 | 100.0 | 108 | 3 AAG01289 | Aag01289 Human sec |
| 13 | 146 | 100.0 | 108 | 3 AAG54610 | Aag54610 Zea may |
| 14 | 146 | 100.0 | 109 | 3 AAG41100 | Aag41100 Zea may |
| 15 | 146 | 100.0 | 110 | 3 AAG27142 | Aag27142 Zea may |
| 16 | 146 | 100.0 | 113 | 3 AAG12241 | Aag12241 Zea may |
| 17 | 146 | 100.0 | 114 | 3 AAG44971 | Aag44971 Zea may |
| 18 | 146 | 100.0 | 117 | 3 AAG12552 | Aag12552 Zea may |
| 19 | 146 | 100.0 | 121 | 3 AAG12629 | Aag12629 Zea may |
| 20 | 146 | 100.0 | 121 | 3 AAG44980 | Aag44980 Zea may |
| 21 | 146 | 100.0 | 126 | 3 AAG12354 | Aag12354 Zea may |
| 22 | 146 | 100.0 | 130 | 3 AAG26892 | Aag26892 Zea may |
| 23 | 146 | 100.0 | 131 | 3 AAG27143 | Aag27143 Zea may |
| 24 | 146 | 100.0 | 134 | 2 AAU07284 | AAU07284 Histone H |
| 25 | 146 | 100.0 | 134 | 2 AAU05482 | AAU05482 Consensus |

| | | | | | |
|----|-----|-------|-----|------------|--------------------|
| 26 | 146 | 100.0 | 135 | 2 AAU07285 | AAU07285 Human his |
| 27 | 146 | 100.0 | 135 | 2 AAU05483 | AAU05483 Human his |
| 28 | 146 | 100.0 | 135 | 7 ADE59324 | AdE59324 Rat Prote |
| 29 | 146 | 100.0 | 136 | 3 AAG43664 | Aag43664 Arabidops |
| 30 | 146 | 100.0 | 136 | 3 AAG47930 | Aag47930 Arabidops |
| 31 | 146 | 100.0 | 136 | 3 AAG07917 | Aag07917 Arabidops |
| 32 | 146 | 100.0 | 136 | 3 AAG41099 | Aag41099 Zea may |
| 33 | 146 | 100.0 | 136 | 3 AAG43813 | Aag43813 Arabidops |
| 34 | 146 | 100.0 | 136 | 3 AAG53143 | Aag53143 Arabidops |
| 35 | 146 | 100.0 | 136 | 3 AAG10324 | Aag10324 Arabidops |
| 36 | 146 | 100.0 | 136 | 3 AAG12084 | Aag12084 Arabidops |
| 37 | 146 | 100.0 | 136 | 3 AAG08768 | Aag08768 Arabidops |
| 38 | 146 | 100.0 | 136 | 3 AAG44415 | Aag44415 Arabidops |
| 39 | 146 | 100.0 | 136 | 3 AAG26219 | Aag26219 Arabidops |
| 40 | 146 | 100.0 | 136 | 3 AAG53145 | Aag53145 Arabidops |
| 41 | 146 | 100.0 | 136 | 3 AAG04323 | Aag04323 Arabidops |
| 42 | 146 | 100.0 | 136 | 3 AAG53099 | Aag53099 Arabidops |
| 43 | 146 | 100.0 | 136 | 4 AAM17089 | Aam17089 Peptide # |
| 44 | 146 | 100.0 | 136 | 4 ABB61842 | Abb61842 Drosophi1 |
| 45 | 146 | 100.0 | 136 | 4 ABB64138 | Abb64138 Drosophi1 |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| ADA13508 | ADA13508 standard; peptide; 30 AA. |
| XX | ADA13508; |
| AC | ADA13508; |
| XX | |
| DT | 20-NOV-2003 (first entry) |
| XX | |
| DE | Human H3 histone amino acid sequence. |
| XX | |
| KW | detection; active gene; inactive gene; antibody; modified histone; |
| KW | tumour suppressor; oncogene; human; histone; epitope. |
| XX | |
| OS | Synthetic. |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FT | Modified-site 2 Location/Qualifiers |
| FT | Modified-site 4 /label= methylation |
| FT | Modified-site 9 /label= methylation |
| FT | Modified-site 10 /label= acetylation or methylation |
| FT | Modified-site 10 /label= phosphorylation |
| FT | Modified-site 14 /label= acetylation |
| FT | Modified-site 17 /label= acetylation |
| FT | Modified-site 18 /label= methylation |
| FT | Modified-site 23 /label= acetylation |
| FT | Modified-site 23 /label= acetylation |
| FT | Modified-site 26 /label= acetylation |
| FT | Modified-site 27 /label= methylation |
| FT | Modified-site 27 /label= methylation |
| FT | Modified-site 28 /label= phosphorylation |
| FT | Modified-site 28 /label= phosphorylation |
| XX | |
| PD | 28-AUG-2003. |
| XX | |
| PD | 19-FEB-2003; 2003WO-US004661. |
| XX | |
| PR | 20-FEB-2002; 2002US-0358325P. |
| PR | 19-MAR-2002; 2002US-0365459P. |

| | |
|----|---|
| XX | CENP-A; centromere-associated histone H3; variant; phosphorylation; H3; mitosis; meiosis; kinase inhibitor; cytostatic; human; cancer; marker. |
| XX | Homo sapiens. |
| XX | Key |
| XX | Location/Qualifiers |
| XX | Modified-site |
| XX | 10 |
| XX | /note= "phosphorylated" |
| XX | Modified-site |
| XX | 28 |
| XX | /note= "phosphorylated" |
| XX | WO200192339-A1. |
| XX | 06-DEC-2001. |
| XX | 31-MAY-2001; 2001WO-US017633. |
| XX | 31-MAY-2000; 2000US-0208261P. |
| XX | (UWV-) UNIV VIRGINIA PATENT FOUND. |
| XX | (SCRI) SCRIPPS RES INST. |
| XX | Allis CD, Sullivan KF, |
| XX | WPI; 2002-114331/15. |
| XX | Novel antibody directed against histone H3-like protein (CENP-A) that is phosphorylated at a specific position in the amino terminal part during mitosis in vivo, useful as marker of mitosis and in diagnostic imaging. |
| XX | Disclosure; Fig 1a; 50pp; English. |
| XX | The invention relates to an antibody, which is directed against amino terminal portion of CENP-A (a unique centromere-associated histone H3 variant) that is phosphorylated (Phos CENP-A) or is unphosphorylated (Un CENP-A). Since CENP-A is selectively phosphorylated in vivo at the amino acid Ser at position 7 in the amino terminus during mitosis, anti-Phos CENP-A antibody is useful as a marker of cell mitosis and meiosis. The antibody which specifically binds to Phos CENP-A and coupled to a bioactive substance such as a drug, toxin, immunomodulator, a peptide effector or an isotope, is useful for treating cancer in humans. The antibody is also useful in screening for potential inhibitors of a kinase. The antibody provides a mitosis and/or proliferation marker that has research and diagnostic potential. Since the amount of detectable Phos CENP-A present in a cell varies throughout the cell cycle, the anti-Phos CENP-A antibody can also be used to determine the mitotic stage of a cell. The anti-Phos CENP-A antibody can be used for identifying tissues that contain a high incidence of mitotic cells and assist in detecting oncogenesis and cancer, and thus is useful for locating and diagnosing cancer in vivo. It can also be used for isolating mitotically dividing cells from complex mixtures. The present sequence represents the amino-terminal sequence of the human histone H3 protein |
| XX | Sequence 40 AA; |
| XX | Query Match |
| XX | 100.0%; Score 146; DB 5; Length 40; |
| XX | Best Local Similarity 100.0%; Pred. No. 3.8e-13; |
| XX | Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0. |
| XX | 1 ARTKOTARKSTGGKAPRKQATKARKKAP 30 |
| XX | 1 ARTKOTARKSTGGKAPRKQATKARKKAP 30 |
| XX | RESULT 4 |
| XX | ADO21832 |
| XX | ID ADO21832 standard; peptide; 40 AA. |
| XX | ADO21832; |
| XX | 12-AUG-2004 (first entry) |
| XX | Human histone H3 N-terminal peptide (SEQ ID 1). |

| | |
|---|--|
| XX | fusion protein reporter; histone modification; cytosstatic; |
| KM | neuroprotective; muscular; virucide; cancer; neurological; |
| KM | muscular disorders; developmental; cell development; toxin; |
| KM | toxic chemical; virus; human; histone H3; N-terminal. |
| OS | Homo sapiens. |
| XX | |
| PH | Key |
| FT | Modified-site |
| FT | Location/Qualifiers |
| FT | 8 /note= "Post-translational modification acetylation site" |
| FT | 14 /note= "Post-translational modification acetylation site" |
| FT | 18 /note= "Post-translational modification acetylation site" |
| FT | 23 /note= "Post-translational modification acetylation site" |
| FT | Modified-site |
| FT | /note= "Post-translational modification acetylation site" |
| XX | |
| PN | WO200404168-A2. |
| PD | |
| PD | 27-MAY-2004. |
| PF | |
| PF | 12-NOV-2003; 2003WO-US036059. |
| PR | |
| PR | 12-NOV-2002; 2002US-0425578P. |
| PR | 05-AUG-2003; 2003US-00634740. |
| XX | |
| PA | (MASI) MASSACHUSETTS INST TECHNOLOGY. |
| XX | |
| PI | Ting AY; |
| XX | |
| XX | WPI; 2004-420310/39. |
| PT | |
| PT | New fusion protein reporter having a core with a histone-modification- |
| PT | specific binding domain conjugated to a histone polypeptide, useful for |
| PT | diagnosing or treating cancer, viral infections, neurological and |
| PT | mucular disorders. |
| XX | |
| PS | Claim 14; SEQ ID NO 1; 96pp; English. |
| CC | |
| CC | The invention relates to a novel fusion protein reporter comprising a |
| CC | core having a histone-modification-specific binding domain conjugated to |
| CC | a histone polypeptide, wherein the core is flanked by donor and acceptor |
| CC | fluorescent moieties. The molecules of the invention demonstrate |
| CC | cytostatic, neuroprotective, muscular and virucide activities and may be |
| CC | useful for the diagnosis and/or treatment of histone modification- |
| CC | associated disorders, such as cancer, neurological disorders, muscular |
| CC | disorders, developmental disorders, cell development disorders and |
| CC | disorders related to exposure to toxins, toxic chemicals or viruses. The |
| CC | current sequence is that of the human histone H3 N-terminal peptide (SEQ |
| CC | ID 1) of the invention. |
| XX | |
| SQ | Sequence 40 AA: |
| | |
| Query Match | 100.0%; Score 146; DB 8; Length 40; |
| Best Local Similarity | 100.0%; Pred. No. 3.8e-13; |
| Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Cy | 1 ARTQTARKSTGGKAPRKQLATTKARSAAP 30 |
| Dd | |
| | 1 ARTQTARKSTGGKAPRKQLATTKARSAAP 30 |
| | |
| RESULT 5 | |
| ID | AU70897 standard; peptide; 55 AA. |
| XX | |
| AC | AU70897; |
| XX | |
| DT | 14-FEB-2002 (first entry) |
| XX | |
| DE | Histone 2A-derived gene delivery peptide #17. |
| XX | |

KM Histone 2A; gene therapy; gene delivery; gene therapy; antisense therapy;
KM nuclear localisation.
XX Synthetic.
OS
XX W0200181370-A2.
XX
XX 01-NOV-2001.
XX
XX 24-APR-2001; 2001WO-EP004621.
XX
XX 24-APR-2000; 2000US-0199153P.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (NOVS) NOVARTIS RES INST.
XX
XX Balicki D, Beutler E;
XX
XX WPI; 2002-055343/07.
XX
XX Histone H2A-derived peptides useful in gene delivery and gene therapy.
XX
XX
XX Example; Fig 1; 37pp; English.
XX
XX The invention relates to an isolated gene delivery facilitating peptide
XX (I) comprising at least 7 amino acids (preferably 17 amino acids) derived
XX from the N-terminal region of Histone H2A, and which exhibits
XX transfection activity and nuclear localisation activity. (I) is useful
XX for delivering a nucleic acid to cells. The gene delivery enhancing
XX peptide, derived from Histone H2A is complexed with a nucleic acid for
XX efficient and stable delivery of the nucleic acid into a cell, ultimately
XX to the nucleus. The peptide mediated positive charges on the histone are bound
XX principle that un-neutralised positive charges on the histone backbone of
XX electro-statically both by the negatively charged phosphate backbone of
XX DNA and that nuclear targeting signals in the histones improve
XX trafficking of the DNA into the nucleus for transfection. This mode of
XX delivery overcomes the limitations of current gene delivery approaches
XX including viral and non-viral means, has minimum toxicity, with cellular
XX access, intracellular trafficking and nuclear retention of plasmids. The
XX entire H2A sequence is not essential for mediating efficient delivery of
XX the nucleic acids into cells as opposed to the sequences have also been
XX sequence. In addition, substitutions to the sequences have also been
XX found to mediate efficient delivery, providing an improved delivery
XX system on the original H2A protein. AAU70877-AAU70923 represent histone
XX 2A-derived gene delivery peptides used in the method of the invention
XX
XX
XX Sequence 55 AA;
XX
XX
XX Query Match 100.0%; Score 146; DB 5; Length 55;
XX Best local similarity 100.0%; Pred. No. 5,3e-13;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ARTKQTARKSTGGKAPKQLATTKARKSAP 30
DB 1 ARTKQTARKSTGGKAPKQLATTKARKSAP 30
RESULT 6
AA007049
ID AA007049 standard; protein; 65 AA.
AC AAG07049;
XX
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 4051.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
OS

XX
XX EP1034405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 23-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 23-APR-1999; 99US-0130891P.
XX 28-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132653P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 14-MAY-1999; 99US-0134768P.
XX 18-MAY-1999; 99US-0134941P.
XX 19-MAY-1999; 99US-0135124P.
XX 20-MAY-1999; 99US-0135353P.
XX 21-MAY-1999; 99US-0135629P.
XX 24-MAY-1999; 99US-0136021P.
XX 25-MAY-1999; 99US-0136392P.
XX 27-MAY-1999; 99US-0136782P.
XX 28-MAY-1999; 99US-0137222P.
XX 01-JUN-1999; 99US-0137528P.
XX 03-JUN-1999; 99US-0137502P.
XX 04-JUN-1999; 99US-0137724P.
XX 07-JUN-1999; 99US-0138094P.
XX 08-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 16-JUN-1999; 99US-0139453P.
XX 17-JUN-1999; 99US-0139492P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
XX 18-JUN-1999; 99US-0139456P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
XX 18-JUN-1999; 99US-0139459P.
XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
XX 18-JUN-1999; 99US-0139462P.
XX 18-JUN-1999; 99US-0139463P.
XX 18-JUN-1999; 99US-0139750P.
XX 18-JUN-1999; 99US-0139763P.
XX 18-JUN-1999; 99US-0139817P.
XX 21-JUN-1999; 99US-0139899P.
XX 22-JUN-1999; 99US-0140353P.
XX 23-JUN-1999; 99US-0140354P.
XX 23-JUN-1999; 99US-0140695P.
XX 24-JUN-1999; 99US-0140823P.
XX 28-JUN-1999; 99US-0140991P.
XX 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-014842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
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DT 19-OCT-1994 (first entry)
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Db 2 ARTKOTARKSTGCAKPKOLATKAKKAP 31

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AC AAG22671;
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DT 17-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 25689.
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KW Protein identification; signal transduction pathway; metabolic pathway;
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termination sequence; corn.
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OS Zea mays subsp. mays.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 146; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 8.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
Dd 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

RESULT 10

ABP42906
ID ABP42906 standard; protein; 93 AA.

AC ABP42906;
DT 22-AUG-2002 (first entry)

XX Human ovarian antigen HPDQX13, SEQ ID NO:4038.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KM inflammatory condition; immune disorder; blood disorder;
KM cardiovascular disorder; respiratory disorder; neurological disorder;
KM gastrointestinal disorder; urinary system disorder; drug screening;
KM gene therapy; chromosome mapping; forensic analysis;
KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KM antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI: 2002-147878/19.

XX N-PSDB; ABO55983.

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
cancer), immune disorders, cardiovascular disorders and neurological
diseases.

XX Claim 11; SEQ ID NO 4038; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP41328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 93 AA;

Query Match 100.0%; Score 146; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

Dd 4 ARTKQTARKSTGGKAPRKQLATKARKSAP 33

RESULT 11

AAG13239
ID AAG13239 standard; protein; 95 AA.

XX AAG13239;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 12660.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 30-APR-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

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PR 26-OCT-1999; 99US-0161360P.
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PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161931P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 146; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 9.3e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARTKOTARKSTGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGKAPRKQLATKARKSAP 31

RESULT 12
ID AAG01289
AAG01289 standard; protein, 108 AA.

AC AAG01289;
XX
DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 5370.

KW Human, 5' EST, expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.

OS Homo sapiens.

PN EPI033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

PR 26-FEB-1999; 99US-0122487P.

PA (GEST) GENSET.

PI Dunas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

DR N-PSDB; AAC01295.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 5370; 71bp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNA or polyA⁺ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 146; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARTKOTARKSTGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGKAPRKQLATKARKSAP 31

RESULT 13
ID AAG54610
AAG54610 standard; protein, 108 AA.

AC AAG54610;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 69649.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

OS Zea mays subsp. mays.

PN EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126254P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 07-MAY-1999; 99US-0132487P.

PR 11-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134370P.

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PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135333P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136382P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

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PR 07-JUN-1999; 99US-0137724P.

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PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 146; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 1, 1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGKAPRKOLATKARKSAP 30
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DB 2 ARTKOTARKSTGKAPRKOLATKARKSAP 31
RESULT 14
AAG41100
ID AAG41100 standard; protein; 109 AA.
AC AAG41100;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 51091.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
FN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0121180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
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GenCore version 5.1.6
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Searched: 1595201 seqs, 359116952 residues

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Listing first 45 summaries

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ALIGNMENTS

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Publication No. US20040102606A1
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APPLICANT: Balicki, Danuta
TITLE OF INVENTION: Histone H2A-derived peptides useful in gene delivery
FILE REFERENCE: T8RI 743.1
CURRENT APPLICATION NUMBER: US/10/258, 637
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: PCT/EP01/04621
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,153
NUMBER OF SEQ ID NOS: 46
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SEQ ID NO 20
LENGTH: 55
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OTHER INFORMATION: synthetic histone-derived peptide
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/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
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/ CURRENT FILING DATE: 2003-04-28
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/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 238920
/ LENGTH: 83
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_149484C.1.pep
US-10-425-115-238920
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Query Match          100.0%; Score 146; DB 17; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 2 ARTKQTARKSTGGKAPPRKQLATKARKSAP 31
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```
RESULT 4
US-10-424-599-282206
/ Sequence 282206, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 265684
/ SEQ ID NO 282206
/ LENGTH: 85
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(85)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_96855C.1.pep
US-10-424-599-282206
```

```
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 265684
/ SEQ ID NO 282206
/ LENGTH: 85
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(85)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_96855C.1.pep
US-10-424-599-282206
```

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Query Match          100.0%; Score 146; DB 15; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 38 ARTKQTARKSTGGKAPPRKQLATKARKSAP 67
```

```
RESULT 5
US-10-425-115-250033
/ Sequence 250033, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 250033
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_159614C.1.pep
US-10-425-115-250033
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```
Query Match          100.0%; Score 146; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 2 ARTKQTARKSTGGKAPPRKQLATKARKSAP 31
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```
RESULT 6
US-10-425-115-218722
/ Sequence 218722, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
```

```
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 218722
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_131066C.1.pep
US-10-425-115-218722

Query Match          100.0%; Score 146; DB 17; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,8e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQTARKSTGGKAPRKQLATKAARKSAP 30
    |||
Db 2 ARTKQTARKSTGGKAPRKQLATKAARKSAP 31

RESULT 7
US-10-425-115-337375
; Sequence 337375, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337375
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70856C.1.pep
US-10-425-115-337375

Query Match          100.0%; Score 146; DB 17; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,8e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQTARKSTGGKAPRKQLATKAARKSAP 30
    |||
Db 35 ARTKQTARKSTGGKAPRKQLATKAARKSAP 64

RESULT 8
US-10-264-049-4038
; Sequence 4038, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Blise et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4038
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (45)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (57)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4038

Query Match          100.0%; Score 146; DB 15; Length 93;
Best Local Similarity 100.0%; Pred. No. 1,9e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQTARKSTGGKAPRKQLATKAARKSAP 30
    |||
Db 4 ARTKQTARKSTGGKAPRKQLATKAARKSAP 33

RESULT 9
US-10-425-115-336777
; Sequence 336777, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 336777
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70288C.1.pep
US-10-425-115-336777

Query Match          100.0%; Score 146; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 1,9e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQTARKSTGGKAPRKQLATKAARKSAP 30
    |||
Db 7 ARTKQTARKSTGGKAPRKQLATKAARKSAP 36

RESULT 10
US-10-425-115-223514
; Sequence 223514, Application US/10425115
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```
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 223514
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_135434C.1.pep
US-10-425-115-223514
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```
Query Match          100.0%; Score 146; DB 17; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
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```
RESULT 11
US-10-425-115-250042
/ Sequence 250042, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 250042
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)-(109)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: MRT4577_159622C.1.pep
US-10-425-115-250042
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Query Match          100.0%; Score 146; DB 17; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
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```
RESULT 12
US-10-424-599-254928
/ Sequence 254928, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
```

```
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 254928
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)-(117)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_72222C.1.pep
US-10-424-599-254928
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Query Match          100.0%; Score 146; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
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```
RESULT 13
US-10-425-115-368708
/ Sequence 368708, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 368708
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_99435C.1.pep
US-10-425-115-368708
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Query Match          100.0%; Score 146; DB 17; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
```

```
RESULT 14
US-10-425-115-333644
/ Sequence 333644, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 333644
 ; LENGTH: 128

; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(128)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_67396C.1.pep
 US-10-425-115-333644

Query Match 100.0%; Score 146; DB 17; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2,7e-12;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQLATKARKSAP 30
 DB 2 ARTKOTARKSTGKAPRKQLATKARKSAP 31

RESULT 15

US-10-425-115-250032
 ; Sequence 250032, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 250032
 ; LENGTH: 130
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(130)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_159613C.1.pep
 US-10-425-115-250032

Query Match 100.0%; Score 146; DB 17; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2,7e-12;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQLATKARKSAP 30
 DB 2 ARTKOTARKSTGKAPRKQLATKARKSAP 31

Search completed: December 23, 2004, 11:39:02
 Job time : 150 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:13:09, Search time 39 Seconds

(Without alignments)
74.013 Million cell updates/sec

Title: US-10-634-740-18

Perfect score: 146
Sequence: 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 146 | 100.0 | 35 | 2 A39525 | histone H3 - mouse |
| 2 | 146 | 100.0 | 39 | 2 I48113 | histone H3.2 - Chi |
| 3 | 146 | 100.0 | 48 | 2 A61286 | histone H3 - sea u |
| 4 | 146 | 100.0 | 48 | 2 C61286 | histone H3 - cycad |
| 5 | 146 | 100.0 | 48 | 2 B61286 | histone H3 - sandp |
| 6 | 146 | 100.0 | 60 | 2 S51664 | histone H3.3 - tom |
| 7 | 146 | 100.0 | 62 | 2 B38309 | histone H3.2 - alf |
| 8 | 146 | 100.0 | 76 | 2 A38309 | histone H3.1 - alf |
| 9 | 146 | 100.0 | 121 | 2 A02610 | histone H3 - bovin |
| 10 | 146 | 100.0 | 135 | 1 HSB03 | histone H3 - bovin |
| 11 | 146 | 100.0 | 135 | 1 HSEAA3 | histone H3 - Alen |
| 12 | 146 | 100.0 | 135 | 1 HSF13 | histone H3 - small |
| 13 | 146 | 100.0 | 135 | 1 HSEW3 | histone H3 - garde |
| 14 | 146 | 100.0 | 135 | 1 HSRK3 | histone H3 - scrif |
| 15 | 146 | 100.0 | 135 | 1 HSTR3 | histone H3 - gonada |
| 16 | 146 | 100.0 | 135 | 1 HSR3M | histone H3, embryo |
| 17 | 146 | 100.0 | 135 | 1 HSTR3P | histone H3, embryo |
| 18 | 146 | 100.0 | 135 | 1 HSKX1 | histone H3.1 - Alf |
| 19 | 146 | 100.0 | 135 | 2 JQ1963 | H3.3 like histone |
| 20 | 146 | 100.0 | 135 | 2 S00373 | histone H3 - wheat |
| 21 | 146 | 100.0 | 136 | 1 HSKW3 | histone H3 - Caeno |
| 22 | 146 | 100.0 | 136 | 1 HSCW3 | histone H3 - chick |
| 23 | 146 | 100.0 | 136 | 1 HSHU3 | histone H3.3 [vali |
| 24 | 146 | 100.0 | 136 | 1 HSHU3 | histone H3.3 [vali |
| 25 | 146 | 100.0 | 136 | 2 AS6580 | histone H3 - midge |
| 26 | 146 | 100.0 | 136 | 2 S10097 | histone H3 - fruit |
| 27 | 146 | 100.0 | 136 | 2 AS6618 | histone H3 - spoon |
| 28 | 146 | 100.0 | 136 | 2 AS6618 | histone H3 - Tigr1 |
| 29 | 146 | 100.0 | 136 | 2 AS6654 | histone H3 - Tigr1 |

| | | | | | |
|----|-----|-------|-----|----------|----------------------|
| 30 | 146 | 100.0 | 136 | 2 S06743 | histone H3 - mouse |
| 31 | 146 | 100.0 | 136 | 2 I49397 | histone H3.2 prote |
| 32 | 146 | 100.0 | 136 | 2 I49398 | histone H3.1 prote |
| 33 | 146 | 100.0 | 136 | 2 I57019 | H3 histone - rat |
| 34 | 146 | 100.0 | 136 | 2 S61218 | histone H3.3 - fru |
| 35 | 146 | 100.0 | 136 | 2 S61220 | histone H3.3 - fru |
| 36 | 146 | 100.0 | 136 | 2 S01198 | histone H3 - starf |
| 37 | 146 | 100.0 | 136 | 2 S20678 | histone H3 - starf |
| 38 | 146 | 100.0 | 136 | 2 I50245 | histone H3.3B - ch |
| 39 | 146 | 100.0 | 136 | 2 S01196 | histone H3 - starf |
| 40 | 146 | 100.0 | 136 | 2 S01197 | histone H3 - starf |
| 41 | 146 | 100.0 | 136 | 2 S20669 | histone H3.3 - starf |
| 42 | 146 | 100.0 | 136 | 2 S50140 | histone H3 - sea |
| 43 | 146 | 100.0 | 136 | 2 JN0687 | histone H3 - sea |
| 44 | 146 | 100.0 | 136 | 2 S10168 | histone H3.3A - ra |
| 45 | 146 | 100.0 | 136 | 2 S56707 | histone H3 homolo |

ALIGNMENTS

RESULT 1

A39525 histone H3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 12-Apr-1995
C:Accession: A39525
R:Mahadevan, L.C.; Willis, A.C.; Barratt, M.J.
Cell 65, 775-783, 1991
A>Title: Rapid histone H3 phosphorylation in response to growth factors, phorbol esters
A:Reference number: A39525; PMID:91249384; PMID:2040014
A:Accession: A39525
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-35 <MA>
C:Superfamily: histone H3
C:Keywords: chromosomal protein; nucleosome core

Query Match 100.0%; Score 146; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
DB 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

RESULT 2

I48113 histone H3.2 - Chinese hamster (fragment)
C:Species: Citicellus griseus (Chinese hamster)
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I48113
R:Artishevsky, A.; Wooden, S.; Sharma, A.; Resendez, E.
Nature 328, 823-827, 1987
A>Title: Cell-cycle regulatory sequences in a hamster histone promoter and their interaction with a cell cycle inhibitor
A:Reference number: I48113; PMID:87315341; PMID:3627229
A:Accession: I48113
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-39 <RS>
A:Cross-references: GB:M28265; NID:9341874; PIND:AAA42371.1; PID:9554580
C:Gene: H3.2
C:Superfamily: histone H3

Query Match 100.0%; Score 146; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
DB 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

RESULT 3

A61286
histone H3 - sea urchin (Parechinus angulosus) (fragment)
C/Species: Parechinus angulosus (angulate urchin)
C/Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C/Accession: A61286
R/Brandt, W.F.; Strickland, W.N.; Morgan, M.; Von Holt, C.
FEBS Lett. 40, 167-172, 1974
A/Title: Comparison of the N-terminal amino acid sequences of histone F3 from a mammal,
A/Reference number: A61286; MUID:7429572; PMID:4851114
C/Accession: A61286
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-48 <BRA>
A/Cross-references: UNIPROT:Q7M327
C/Superfamily: histone H3

Query Match 100.0%; Score 146; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 4

C61286
histone H3 - cycad (Encephalartos caffer) (fragment)
C/Species: Encephalartos caffer (cycad)
C/Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C/Accession: C61286
R/Brandt, W.F.; Strickland, W.N.; Morgan, M.; Von Holt, C.
FEBS Lett. 40, 167-172, 1974
A/Title: Comparison of the N-terminal amino acid sequences of histone F3 from a mammal,
A/Reference number: A61286; MUID:7429572; PMID:4851114
C/Accession: C61286
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-48 <BRA>
A/Cross-references: UNIPROT:Q7M1P0
C/Superfamily: histone H3

Query Match 100.0%; Score 146; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 5

B61286
histone H3 - sandpaper limpet (fragment)
C/Species: Patella granatina (sandpaper limpet)
C/Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C/Accession: B61286
R/Brandt, W.F.; Strickland, W.N.; Morgan, M.; Von Holt, C.
FEBS Lett. 40, 167-172, 1974
A/Title: Comparison of the N-terminal amino acid sequences of histone F3 from a mammal,
A/Reference number: A61286; MUID:7429572; PMID:4851114
C/Accession: B61286
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-48 <BRA>
A/Cross-references: UNIPROT:Q7M328
C/Superfamily: histone H3

Query Match 100.0%; Score 146; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 6

S51664
histone H3.3 - tomato (fragment)
C/Species: Lycopersicon esculentum (tomato)
C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Jul-1998
C/Accession: S51664
R/Hartung, F.
Submitted to the EMBL Data Library, December 1994
A/Reference number: S51664
A/Accession: S51664
A/Molecule type: mRNA
A/Residues: 1-60 <HAR>
A/Cross-references: EMBL:X83422
A/Experimental source: cultivar Rutgers; clone Y17-3
C/Superfamily: histone H3
C/Keywords: DNA binding

Query Match 100.0%; Score 146; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKARKSAP 31

RESULT 7

B38309
histone H3.2 - alfalfa (fragments)
C/Species: Medicago sativa (alfalfa)
C/Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C/Accession: B38309
R/Waterborg, J.H.
J. Biol. Chem. 265, 17157-17161, 1990
A/Title: Sequence analysis of acetylation and methylation in two histone H3 variants of
A/Reference number: A38309; MUID:91009145; PMID:2211618
C/Accession: B38309
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-62 <WAT>
A/Cross-references: UNIPROT:P11105
C/Superfamily: histone H3
C/Keywords: chromosomal protein; DNA binding; nucleosome core; nucleu

Query Match 100.0%; Score 146; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30
Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 8

A38309
histone H3.1 - alfalfa (fragments)
C/Species: Medicago sativa (alfalfa)
C/Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C/Accession: A38309
R/Waterborg, J.H.
J. Biol. Chem. 265, 17157-17161, 1990
A/Title: Sequence analysis of acetylation and methylation in two histone H3 variants of
A/Reference number: A38309; MUID:91009145; PMID:2211618
C/Accession: A38309
A/Status: preliminary
A/Molecule type: protein

A:Residues: 1-76 <MAT>
A:Cross-references: UNIPROT:P02300
C:Superfamily: histone H3
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 100.0%; Score 146; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30
DB 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30

RESULT 9

A02630
histone H3 - fruit fly (*Drosophila melanogaster*) (fragments)
C:Species: *Drosophila melanogaster*
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02630
R:Goldberg, M.L.
Ph.D. thesis, Stanford Univ., 1979
A:Reference number: A02630
A:Accession: A02630
A:Molecule type: DNA
A:Residues: 1-121 <GOL>
A:Cross-references: UNIPROT:P02299
A:Note: the author translated the codon CCC for residue 31 as Ala
C:Genetics:
A:Gene: FLYBase:H33
A:Cross-references: FLYBase:FBgn0001199
C:Superfamily: histone H3
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 100.0%; Score 146; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.5e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30
DB 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30

RESULT 10

HSEB03
histone H3 - bovine
C:Species: *Bos primigenius taurus* (cattle)
C>Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C:Accession: A02624; PLO130; R49978; S68319
R:Delange, R.J.; Hooper, J.A.; Smith, E.L.
J. Biol. Chem. 248, 3261-3274, 1973
A:Title: Histone III. III. Sequence studies on the cyanogen bromide peptides; complete a
A:Reference number: A92132; PMID:7316574; PMID:4735580
A:Accession: A02624
A:Molecule type: protein
A:Residues: 1-135
A:Cross-references: UNIPROT:P16106
A:Note: Cys-96 and Cys-110 can form an intrachain disulfide bond or interchain disulfide
A:Note: Lys-23 is acetylated in 43% of the molecules and Lys-14, in an unknown percent
R:Partridge, W.M.; Nowlin, D.M.; Calaycay, J.; Shively, J.E.
J. Neurochem. 53, 1014-1018, 1989
A:Title: Predominant low-molecular-weight proteins in isolated brain capillaries are his
A:Reference number: PLO130; PMID:85361419; PMID:2769252
A:Accession: PLO130
A:Molecule type: protein
A:Residues: 1-16 <PAR>
A:Experimental source: brain
R:Makim, B.T.; Aswad, G.D.
J. Biol. Chem. 269, 2722-2727, 1994
A:Title: Ca(2+)-calmodulin-dependent phosphorylation of arginine in histone 3 by a nucle
A:Reference number: A49978; PMID:94132040; PMID:8300603
A:Accession: A49978
A:Molecule type: protein

A:Residues: 1-24;121-135 <WAK>
R:Delange, R.J.; Smith, E.L.
J. Biol. Chem. 248, 3248-3254, 1973
A:Title: Histone III. I. Isolation and sequences of the tryptic peptides from the maley
A:Reference number: A92130; PMID:7316572; PMID:4735579
A:Contents: annotation; tryptic peptides
R:Hooper, J.A.; Smith, E.L.
J. Biol. Chem. 248, 3255-3260, 1973
A:Title: Histone III. II. Isolation and sequences of chymotryptic peptides from calf th
A:Reference number: A92131; PMID:7316573; PMID:4700459
A:Contents: annotation; chymotryptic peptides
R:Marzluft Jr., W.F.; Sanders, L.A.; Miller, D.M.; McCarty, K.S.
J. Biol. Chem. 247, 2026-2033, 1972
A:Title: Two chemically and metabolically distinct forms of calf thymus histone F3.
A:Reference number: A92102; PMID:72154496; PMID:5016641
A:Contents: annotation; thymus; variant
A:Note: 20% of the histone H3 fraction consists of a minor form that differs from that
R:Patthy, L.; Smith, E.L.
J. Biol. Chem. 250, 1919-1920, 1975
A:Title: Histone III. IV. Two forms of calf thymus histone III.
A:Reference number: A92174; PMID:75095680; PMID:1167550
A:Contents: annotation; variant
A:Note: analyses of two chymotryptic peptides, both corresponding to positions 91-99, i
R:Coupez, M.; Belatche, D.
Arch. Biochem. Biophys. 325, 29-38, 1996
A:Title: Successive elution by ion-exchange chromatography of H3-H4 histone complexes d
A:Reference number: S68319; PMID:96140594; PMID:8554340
A:Accession: S68319
A:Molecule type: protein
A:Residues: 1-29 <COU>
C:Superfamily: histone H3
C:Keywords: acetyllysine; chromosomal protein; DNA binding; methylated amino acid; nucl
F:2,128,129,131/Binding site: phosphate (Arg) (covalent) #status experimental
F:9,27/Modified site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6,N6-trimethyllysine
F:14,23/Binding site: acetyl (Lys) (covalent) (partial) #status experimental
F:96,110/Disulfide bonds: interchain (in polymeric form) #status experimental
F:96-110/Disulfide bonds: (in monomeric form) #status experimental

Query Match 100.0%; Score 146; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30
DB 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30

RESULT 11

HSEAH3
histone H3 - *Altenstein's bread tree*
C:Species: *Enecephalartos altensteinii* (*Altenstein's bread tree*)
C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A23604
R:Brandt, W.F.; von Holt, C.
FEBS Lett. 194, 278-281, 1986
A:Title: The primary structure of histone H3 from cycad pollen.
A:Reference number: A23604
A:Accession: A23604
A:Molecule type: protein
A:Residues: 1-135 <BRA>
A:Cross-references: UNIPROT:P08903
A:Experimental source: pollen
A:Note: 53-Lys, 96-Ser, 107-Ser, and 124-Val were also found
C:Superfamily: histone H3
C:Keywords: chromosomal protein; DNA binding; methylated amino acid; nucleosome core
F:4/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #status expe
F:9,27/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) #status experimenta

Query Match 100.0%; Score 146; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 12

HSR13

histone H3 - smallmouth buffalo fish

C/Species: Ictiobus bubalus (smallmouth buffalo fish)

C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C/Accession: A02627

R/Hooper, J.A.; Smith, E.L.; Sommer, K.R.; Chalkley, R.

J. Biol. Chem. 248, 3275-3279, 1973

A/Title: Histone III. IV. Amino acid sequence of histone III of the testes of the carp.

A/Reference number: A02627; PMID:7316575; PMID:4700460

A/Accession: A02627

A/Molecule type: protein

A/Residues: 1-135 <HOO>

A/Cross-references: UNIPROT:P16105

A/Note: Lys-9 is epsilon-N-monomethyllysine, epsilon-N-dimethyllysine, epsilon-N-trimeth

A/Note: Lys-27 is epsilon-N-monomethyllysine, epsilon-N-dimethyllysine, epsilon-N-trimeth

C/Superfamily: histone H3

C/Keywords: chromosomal protein; DNA binding; methylated amino acid; nucleosome core

F/9,27/Modified site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6,N6-trimethyllysine

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 13

HSPM3

histone H3 - garden pea (tentative sequence)

C/Species: Pisum sativum (garden pea)

C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004

C/Accession: A02631

R/Patthy, L.; Smith, E.L.; Johnson, J.

J. Biol. Chem. 248, 6834-6840, 1973

A/Title: Histone III. V. The amino acid sequence of pea embryo histone III.

A/Reference number: A02631; PMID:74011270; PMID:4795661

A/Accession: A02631

A/Molecule type: protein

A/Residues: 1-135 <PXT>

A/Cross-references: UNIPROT:P02300

A/Experimental source: embryo

A/Note: Lys-9 and Lys-27 are mainly epsilon-N-monomethyllysine. In a small fraction of

C/Superfamily: histone H3

C/Keywords: chromosomal protein; DNA binding; nucleosome core

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 14

HSRK3

histone H3 - striped catshark

C/Species: Poroderma africanum (striped catshark)

C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C/Accession: A02626

R/Brandt, W.F.; Strickland, W.N.; von Holt, C.

FEBS Lett. 40, 349-352, 1974

A/Title: The primary structure of histone F3 from shark erythrocytes.

A/Reference number: A02626; PMID:74309063; PMID:4855011

A/Accession: A02626

A/Molecule type: protein

A/Residues: 1-135 <BRA>

A/Cross-references: UNIPROT:P16105

A/Note: Lys-9 (70%), Lys-27 (50%), and Lys-36 (20%) are methylated, mainly with the dim

C/Comment: The amount and position of acetylation was not precisely determined. Electroy

C/Superfamily: histone H3

C/Keywords: acetyllysine; chromosomal protein; DNA binding; methylated amino acid; nucl

F/9,27,36/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #statu

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

RESULT 15

HSR13

histone H3, gonadal - rainbow trout

C/Species: Oncorhynchus mykiss (rainbow trout)

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C/Accession: B92959; B93779; B23220

R/Connor, W.; States, J.C.; Mezquita, J.; Dixon, G.H.

J. Mol. Evol. 20, 236-250, 1984

A/Title: Organization and nucleotide sequence of rainbow trout histone H2A and H3 genes

A/Reference number: A92959; PMID:85083109; PMID:6439879

A/Accession: B92959

A/Molecule type: DNA

A/Residues: 1-135 <CON>

A/Cross-references: UNIPROT:P16105; GB:X01064; NID:G64324; PIDN:CMA25529.1; PID:G64326

A/Note: Initiator Met not shown

R/Candido, E.P.M.; Dixon, G.H.

Proc. Natl. Acad. Sci. U.S.A. 69, 2015-2019, 1972

A/Title: Amino-terminal sequences and sites of in vitro acetylation of trout-testis histc

A/Reference number: A93779; PMID:72259090; PMID:4506069

A/Accession: B93779

A/Molecule type: protein

A/Residues: 1-25 <CAN>

C/Superfamily: histone H3

C/Keywords: acetyllysine; chromosomal protein; DNA binding; nucleosome core; testis

F/9,18/Binding site: acetyl (Lys) (covalent) (partial) #status experimental

F/14,23/Binding site: acetyl (Lys) (covalent) #status experimental

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Search completed: December 23, 2004, 11:22:49

Job time : 40 secs